

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2017/07/17 18:18:06*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/bethany/projects/planctomycetes/QC/Gem_obs_UQM2246.sorted.ba
m -c -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	blasr /home/bethany/projects/planctomycet es/pacbio_raw/B08_1/Analysis_Resul ts/m150621_142644_42153_c10080 3462550000001823177910081542_s 1_p0.bas.h5 /home/bethany/projects/planctomycet es/assembly/final_contigs/Gem_obs_ UQM2246_final_contigs.fasta --sam - -nproc 16 --out Gem_obs_UQM2246.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	1 (5.3.574e1c2)
Analysis date:	Mon Jul 17 18:15:46 NZST 2017
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/bethany/projects/planctomycet es/QC/Gem_obs_UQM2246.sorted.b am

## 2. Summary

### 2.1. Globals

Reference size	8,994,052
Number of reads	227,848
Mapped reads	227,848 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	43 / 36,386 / 9,544.07
Duplicated reads (estimated)	56,743 / 24.9%
Duplication rate	9.31%
Clipped reads	227,843 / 100%

### 2.2. ACGT Content

Number/percentage of A's	155,890,500 / 16.95%
Number/percentage of C's	296,108,338 / 32.2%
Number/percentage of T's	155,072,527 / 16.86%
Number/percentage of G's	295,998,035 / 32.18%
Number/percentage of N's	0 / 0%
GC Percentage	64.38%

### 2.3. Coverage

Mean	106.5981
Standard Deviation	51.4528

### 2.4. Mapping Quality

Mean Mapping Quality	221.64
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## 2.5. Mismatches and indels

General error rate	16.91%
Insertions	77,525,409
Mapped reads with at least one insertion	99.77%
Deletions	35,517,466
Mapped reads with at least one deletion	98.96%
Homopolymer indels	18.5%

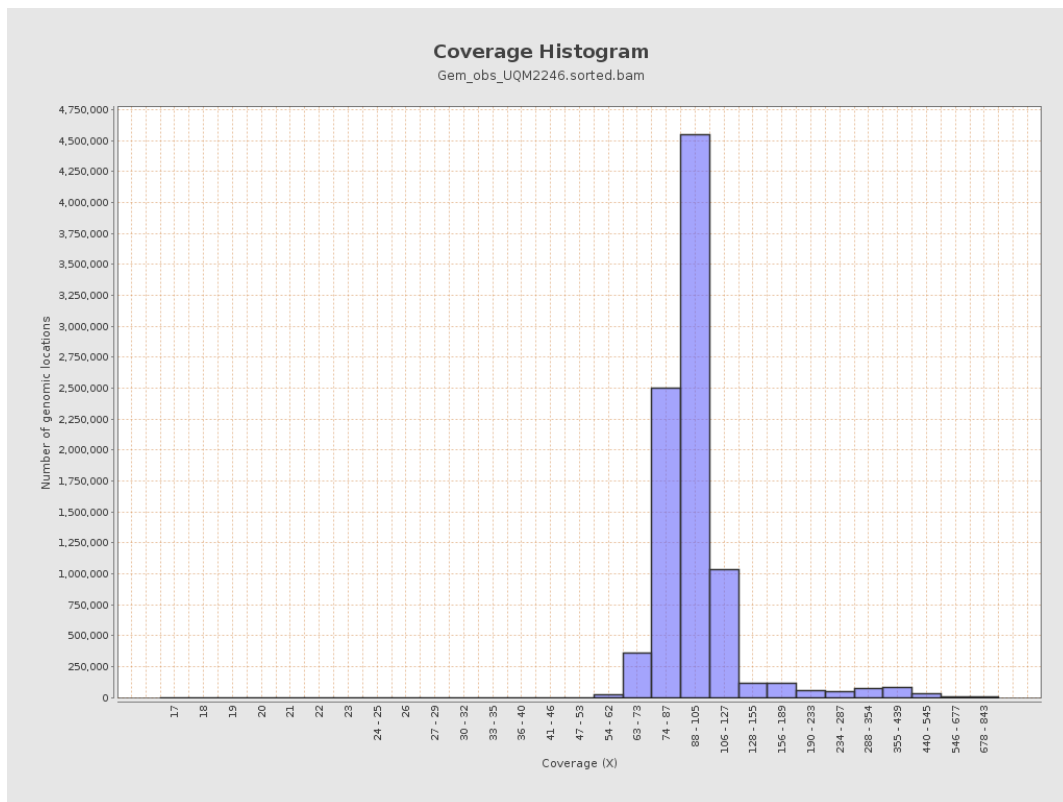
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
contig01	8994052	958748799	106.5981	51.4528

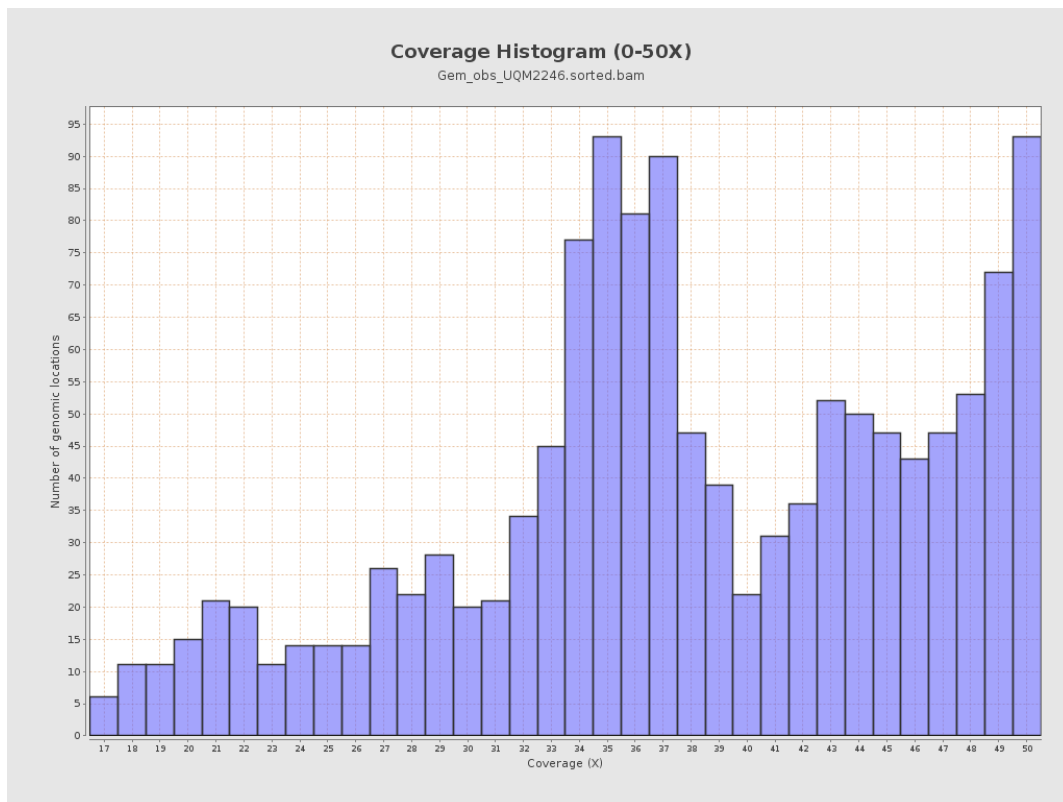
### 3. Results : Coverage across reference



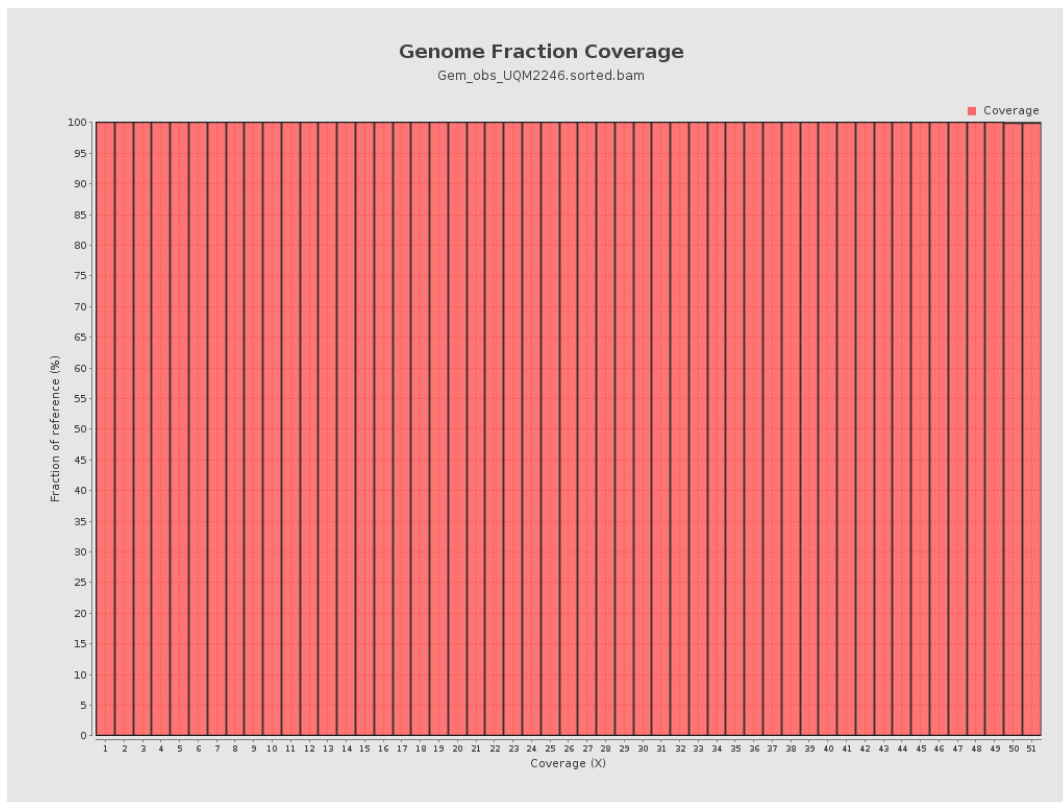
## 4. Results : Coverage Histogram



## 5. Results : Coverage Histogram (0-50X)

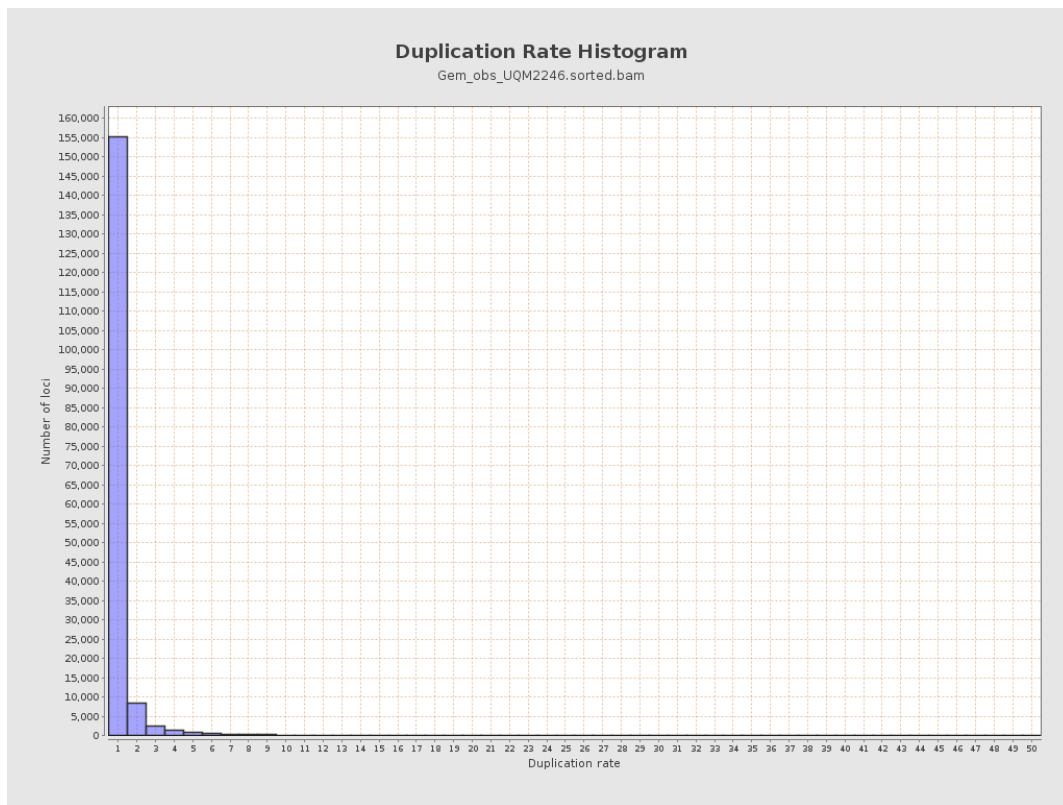


## 6. Results : Genome Fraction Coverage

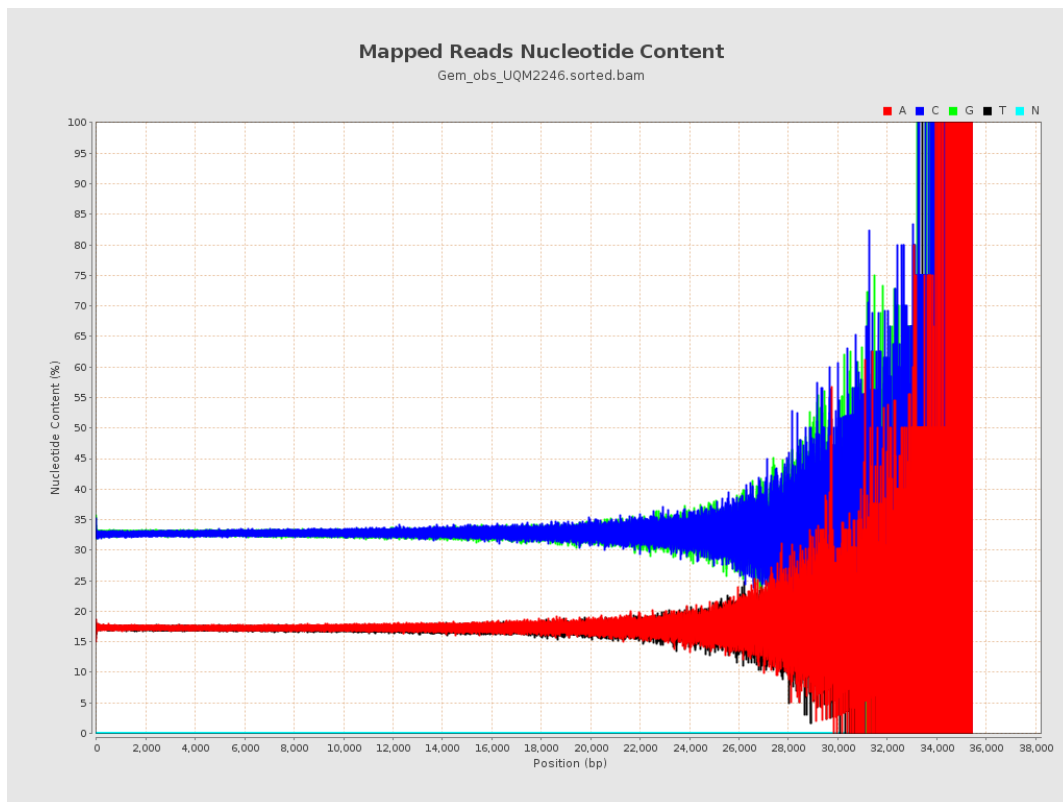




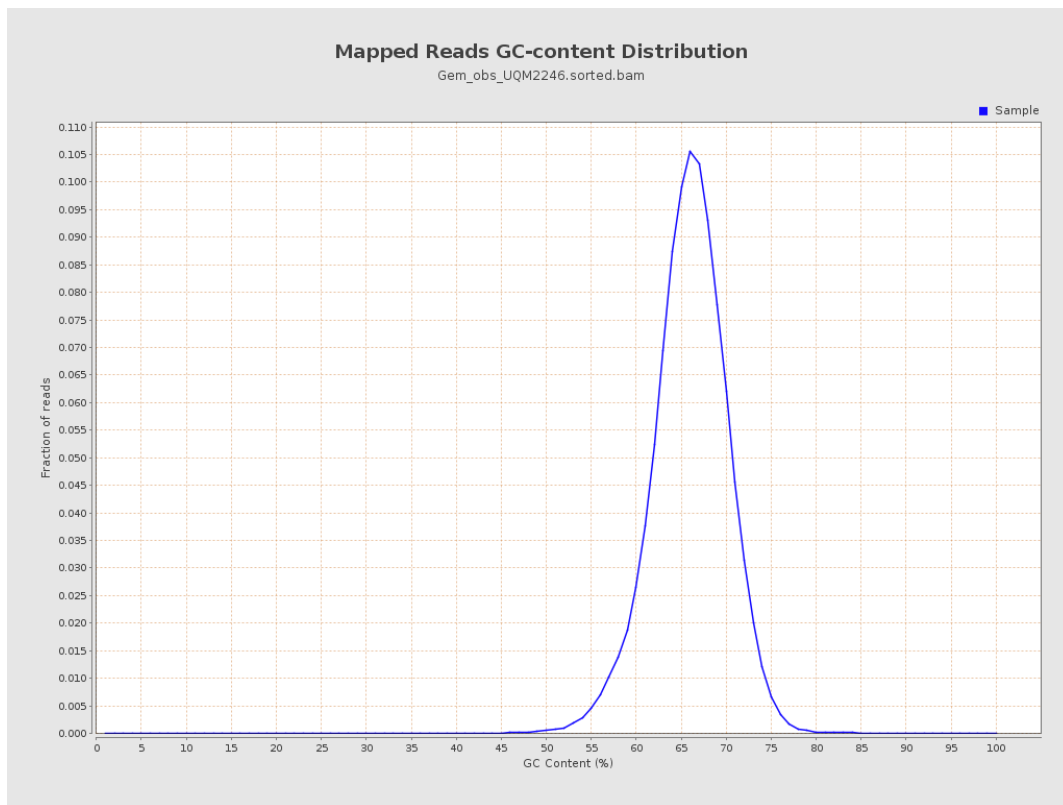
## 7. Results : Duplication Rate Histogram



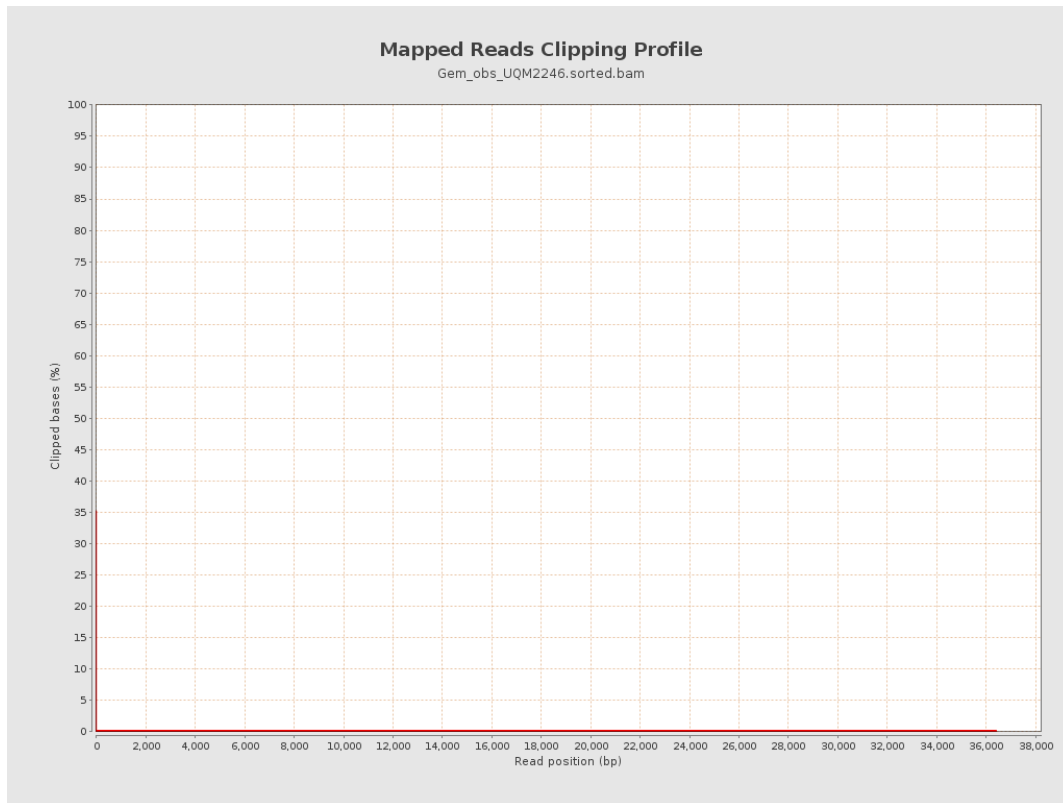
## 8. Results : Mapped Reads Nucleotide Content



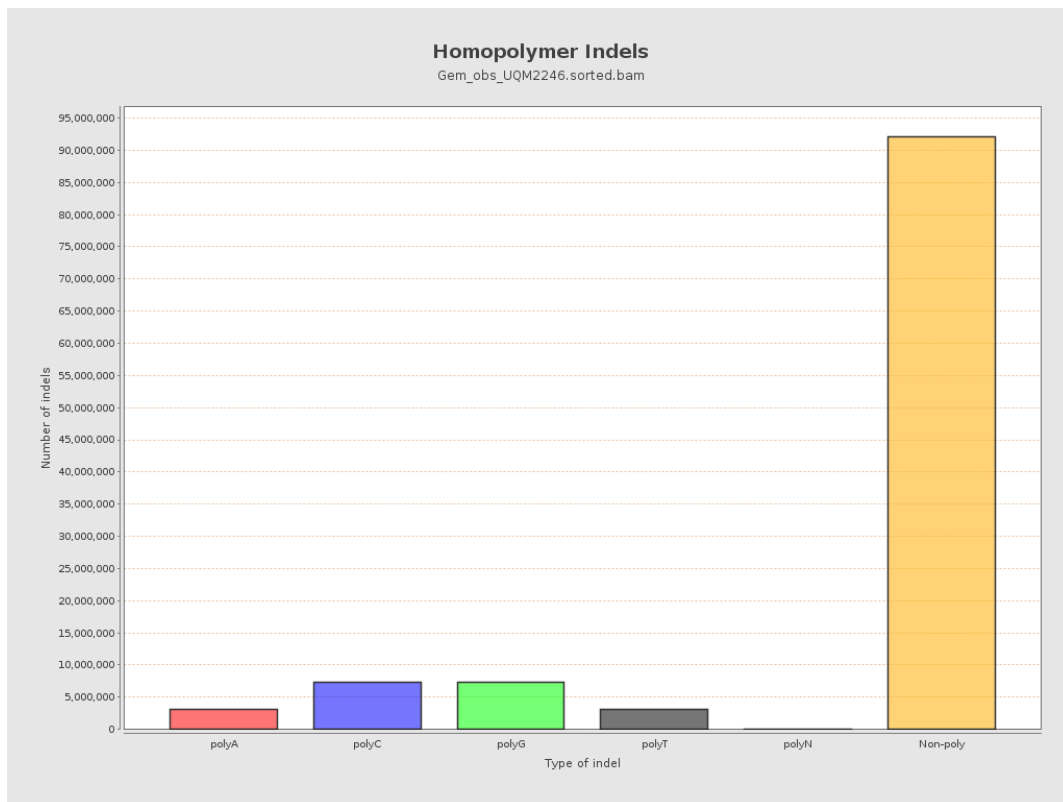
## 9. Results : Mapped Reads GC-content Distribution



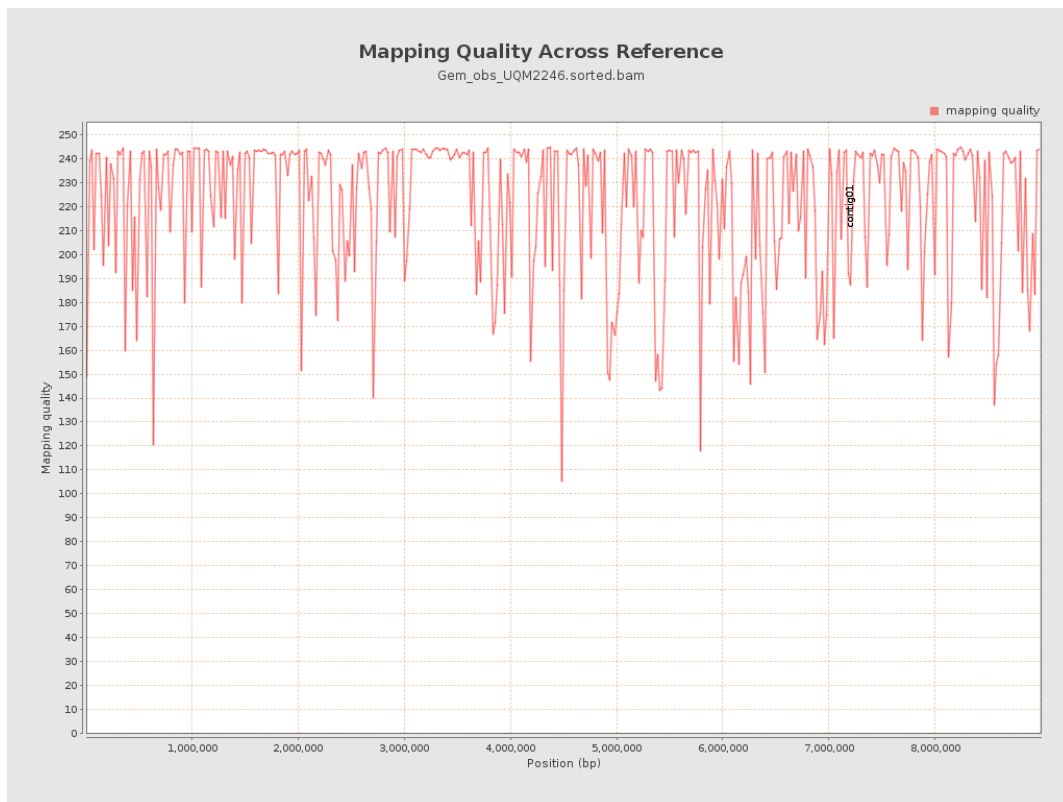
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

